

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 17, 2001, 19:58:43 ; Search time 1216.64 Seconds
(without alignments)
12440.963 Million cell updates/sec

Title: US-09-456-306-1
Perfect score: 2160
Sequence: 1 tttagggcgatctctgtgag.....ggtgccatgagatgcct 2160

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_esthum21:*
64: em_esthum22:*
65: em_esthum23:*
66: em_esthum24:*
67: em_esthum25:*
68: em_esthum26:*
69: em_esthum27:*
70: em_esthum28:*
71: em_esthum29:*
72: em_esthum30:*
73: em_esthum31:*
74: em_esthum32:*
75: em_esthum33:*
76: em_esthum34:*
77: em_esthum35:*
78: em_esthum36:*
79: em_esthum37:*
80: em_esthum38:*
81: em_esthum39:*
82: em_esthum40:*
83: em_esthum41:*
84: em_esthum42:*
85: em_esthum43:*
86: em_esthum44:*
87: em_esthum45:*
88: em_esthum46:*
89: em_esthum47:*
90: em_esthum48:*
91: em_esthum49:*
92: em_esthum50:*
93: em_esthum51:*
94: em_esthum52:*
95: em_esthum53:*
96: em_esthum54:*
97: em_esthum55:*
98: em_esthum56:*
99: em_esthum57:*
100: em_esthum58:*
101: em_esthum59:*
102: em_esthum60:*
103: em_esthum61:*
104: em_esthum62:*
105: em_esthum63:*
106: em_esthum64:*
107: em_esthum65:*
108: em_esthum66:*
109: em_esthum67:*
110: em_esthum68:*
111: em_esthum69:*
112: em_esthum70:*
113: em_esthum71:*
114: em_esthum72:*
115: em_esthum73:*
116: em_esthum74:*

117: em_estp16:*
 118: em_estp17:*
 119: em_estp18:*
 120: em_estp19:*
 121: em_estp20:*
 122: em_estp21:*
 123: em_estp22:*
 124: em_estp23:*
 125: em_estp24:*
 126: em_estp25:*
 127: em_estp26:*
 128: em_estp27:*
 129: em_estp28:*
 130: em_estp29:*
 131: em_estp30:*
 132: em_estp31:*
 133: em_estp32:*
 134: em_estp33:*
 135: em_estp34:*
 136: em_estp35:*
 137: em_estp36:*
 138: em_estp37:*
 139: em_estp38:*
 140: em_estp39:*
 141: em_estp40:*
 142: em_estp41:*
 143: em_estp42:*
 144: em_estp43:*
 145: em_estp44:*
 146: em_estp45:*
 147: em_estp46:*
 148: em_estp47:*
 149: em_estp48:*
 150: em_estp49:*
 151: em_estp50:*
 152: em_estp51:*
 153: em_estp52:*
 154: em_estp53:*
 155: em_estp54:*
 156: em_estp55:*
 157: em_estp56:*
 158: em_estp57:*
 159: em_estp58:*
 160: em_estp59:*
 161: em_estp60:*
 162: em_estp61:*
 163: em_estp62:*
 164: em_estp63:*
 165: em_estp64:*
 166: em_estp65:*
 167: em_estp66:*
 168: em_estp67:*
 169: em_estp68:*
 170: em_estp69:*
 171: em_estp70:*
 172: em_estp71:*
 173: em_estp72:*
 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	95.8	4.4	538	39	AM036130
C 2	69.8	3.2	467	39	AM036129
3	59.2	2.7	475	16	AI097766
4	59.2	2.7	504	27	AI931656
5	59.2	2.7	827	29	AU079796
6	58	2.7	539	87	AM217660
7	57.6	2.7	845	106	BE282914
8	55.8	2.6	492	4	AA289922
9	55.8	2.6	571	22	AI573836
10	54.2	2.5	451	95	AM763503
11	53.2	2.5	612	39	AM035982
12	51.6	2.4	604	94	AM737588
13	51.6	2.4	636	39	AM031597
14	51.6	2.4	644	39	AM033050
15	51.2	2.4	523	111	BE681144
16	50.8	2.4	482	28	AL383545
17	50.8	2.4	520	93	AM684434
18	50	2.3	560	137	BE924524
19	49.4	2.3	824	134	BE037543
20	48.2	2.2	466	1	AA071233
21	47.8	2.2	357	109	BE521719
22	47.8	2.2	490	105	BE194893
23	47.8	2.2	508	40	AM132431
24	47.2	2.2	565	95	AM776566
25	47.2	2.2	462	106	BE264847
26	47	2.2	467	106	BE305099
27	47	2.2	497	105	BE249896
28	47	2.2	533	5	AA306411
29	47	2.2	527	106	BE305023
30	47	2.2	585	106	BE305054
31	47	2.2	604	97	AM958734
32	47	2.2	633	108	BE435274
33	47	2.2	771	107	BE408527
34	47	2.2	835	137	BE894277
35	47	2.2	906	105	BE250242
36	47	2.2	948	105	BE250290
37	47	2.2	985	105	BE250061
38	46.6	2.2	510	4	AA254902
39	46.6	2.2	588	87	AM224881
40	46	2.1	466	143	R17722
41	45.6	2.1	447	12	AA797013
42	45.6	2.1	536	108	BE450711
43	45.6	2.1	561	108	BE449771
44	45.6	2.1	653	24	AT775804
45	45.2	2.1	544	110	BE637311

ALIGNMENTS

RESULT 1
 AM036130/c
 LOCUS
 DEFINITION
 AM036130
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE

538 bp
 mRNA
 EST
 15-SEP-1999
 similar to pyruvate oxidase, mRNA sequence.
 tomato.

ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 538)
AUTHORS Alcalá,J., Vrebalov,J., White,R., Materu,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,M., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
S.D. and Giovannoni,J.
Generation of ESTs from tomato seed tissue
TITLE Unpublished (1999)
JOURNAL Contact: David Fritsch
COMMENT Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfritsch@CLEMSON.EDU
FEATURES
source 1..538
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="T496"
/db_xref="taxon:4081"
/clone="CLE1G11"
/clone_1lb="tomato seed, TAMU"
/tissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
BASE COUNT 109 a 154 c 156 g 119 t
ORIGIN
Query Match 4.4%; Score 95.8; DB 39; Length 538;
Best Local Similarity 53.6%; Pred. No. 1,8e-17;
Matches 199; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
QY 465 cgaatgaagaagcggcggtgtgcaagcgggtgcgaatcgtlgtacactggggaagcgtg 524
DB 533 CCCACGATTAAGTGGCGCTTTCGCGCTGAGACACAACTAGCGTAGAAGT 474
QY 525 gcaagatgagcgtctctgtgtgtctgtgaagaacacacactgattcaaggtctttatgt 564
DB 473 GCGGCTTGGCGGATCGTGGGCCCGGCACTGCACTTAATCAACGGCTTTCGAT 414
QY 585 tgcacatgaatggtgtgcgaagtggtgcacatgcagcatatccgagtgccagatt 644
DB 413 TGCACACCAATCACCCTTCCGCTACTGCGGATGTCGCGCTATTTCCCTCCACGCAAT 354
QY 645 ggtcgaagctcctccagaagaacgcatccgagattgtltaagaagatgctcgtgtac 704
DB 353 GCGACGCGCTATTTCCAGGAACCCACCAAGAGCTATTCCGCAATGTAAGTACTACTAT 294
QY 705 tgcgagatgtgaatgtgtgtgtgagcaggtgtgaacgcatlgtatcagcagatcagtc 764
DB 293 TCGGACTGCTTCCAGCCCGGAGAGATCCCAAGTACTGCGATTGCCATGCCAANA 234
QY 765 accatggcgggttaaaaggtgtgtcgtgtgtagtgaatcgtgtgatatccgtaagaagac 824
DB 233 GCGGCTTCAACCGTGGCTTTCGCTTTCGCTTTCACCAAGCCACGCTGACCTTAACACCT 174
QY 825 gcaagtgacag 835
DB 173 GCGCCAGAAAG 163
RESULT 2
AW036129/c AM036129 467 bp mRNA EST 15-SEP-1999

DEFINITION EST274505 tomato seed, TAMU Lycopersicon esculentum cDNA clone
CLE1G23 similar to pyruvate oxidase, mRNA sequence.
ACCESSION AM036129
VERSION AM036129.1 GI:5894808
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 467)
AUTHORS Alcalá,J., Vrebalov,J., White,R., Materu,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,M., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
S.D. and Giovannoni,J.
Generation of ESTs from tomato seed tissue
TITLE Unpublished (1999)
JOURNAL Contact: David Fritsch
COMMENT Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfritsch@CLEMSON.EDU
FEATURES
source 1..467
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="T496"
/db_xref="taxon:4081"
/clone="CLE1G23"
/clone_1lb="tomato seed, TAMU"
/tissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; CLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBluescript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
BASE COUNT 98 a 134 c 132 g 103 t
ORIGIN
Query Match 3.2%; Score 69.8; DB 39; Length 467;
Best Local Similarity 51.8%; Pred. No. 1,1e-09;
Matches 158; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
QY 531 tgtctgctctctgtgtgtctcgtgaagaacacacactgattcaaggtctltaagtcgcat 590
DB 467 TGGCGCGATCGTGGCGCCCGGCAACCTGCACTTAATCAACGGCTTTCGATTTGCCAC 408
QY 591 cgaatggtgtgcgaagtggtgtgcacatgcgtacgcatatccgagtgccagattgtgtcg 650
DB 407 CGCAATCAGGTTCCGCTACTGCGGATGTCGCTCATATTTCCCTCCAGTGAATTTGCCAGC 348
QY 651 acgtcttcagaagaacgcatccgagattgtltaagaagatgctcgtgttacttcgag 710
DB 347 GCGTATTTCCAGGAACCCACCAAGAGCTATTCCGCAATGTAAGTACTACTATTTGCGAG 288
QY 711 atggtgaatgtgtgtgagcaggtgtgaacgcatlgtatcagcagatcagtcacacatg 770
DB 287 CTGGTTTCAGCCCGGAGAGATCCCAAGTACTGCGGATTTCCATGCGCAAGCGGTG 228
QY 771 gcggttaaaaggtgtgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 830
DB 227 CTAGCGGTGGCGCTTTCGCTTTCGCTTTCACCAAGCGAGCTGCGCTTAACCTGGCGCA 168
QY 831 gacag 835
DB 167 GAAGG 163
RESULT 3

481 cggcgttcgcagccgcgtgcgcgaatcgttatcatcacttggtgagctgcgaagtatgtctgctt 540

BASE COUNT	117 a	114 c	150 g	123 t
ORIGIN				

```

/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNDC-4767"
/clone_lib="Sugano mouse brain mncb"
/sex="female"
/dev_stage="adult"
/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
ATGTCGCCCTTTTCTTTTTTTTTTTT"; double-stranded cDNA was
ligated to a DraIII adaptor (TCGTCGCCCTACTG), digested and
cloned into distinct DraIII sites of the pME18S-FL3. XhoI
sites just outside the DraIII sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al. (University of Tokyo, Institute of Medical Science).

```

/organism="Lycopersicon esculentum"
/cultivar="AA496"
/db_xref="taxon:4081"
/clone="CROC1K5"
/clone_lib="tomato flower buds 8 mm to pre-anthesis
Cornell University"
/tissue_type="flower"

Note: Organ: lung; Vector: pCMV-SORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:74894"
/clone_lib="Soares mouse NML"
/tissue_type="Liver"

```


FEATURES

Location/Quali

source

1. .604
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CT030319"
/clone_1lb="tomato flower buds, anthesis, Cornell University"
/tissue_type="flower"
/dev_stage="anthesis"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

BASE COUNT 138 a 154 c 131 g 181 t

ORIGIN

Query Match 2.4%; Score 51.6; DB 94; Length 604;
Best Local Similarity 51.8%; Pred. No. 0.00033;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 446 tattgagtggtgacgttcgaatgaggaagcggttcgacccggtgcgaatc 505
|||||
Db 372 TATTGTAATGTGCTGCCACATGAAAGGTTGTGTCTGCTCAGAGGTTACGC 431
QY 506 gtgatcacctgggagctgacgatgctgtctctgtgtcctggaacacacacct 565
|||||
Db 432 ACGGCTACTGCGTCCCTGCTTCTATTGCTACATGCTGCTCGGAGCTACGAATCT 491
QY 566 gattcagagttctatgattcgacatcgaaatggtcgaaagtgltggtccatcgatgca 625
|||||
Db 492 TGTTAGCGGCTGCTGCTGCTTGTGTGATAGATCCCATTTGCTATTACCGGTCA 551
QY 626 tattcagagtgccagattggttcgaagcttctccagaaacgcat 671
|||||
Db 552 AGTGCCGAGGAGATGATGTGCTGATGCTTCAAGAACTCTCT 597

RESULT 13
AM031597 636 bp mRNA EST 15-SEP-1999
LOCUS EST275051 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC18E17, mRNA sequence.
ACCESSION AM031597
VERSION AM031597.1 GI:5890353
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 636)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D., and Giovannoni,J. Generation of ESTs from tomato callus tissue Unpublished (1999)
CONTACT: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prime sequence.
FEATURES
source
1. .636
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC18E17"
/clone_1lb="tomato callus, TAMU"

/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni Laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 153 a 161 c 135 g 187 t

ORIGIN

Query Match 2.4%; Score 51.6; DB 39; Length 636;
Best Local Similarity 51.8%; Pred. No. 0.00034;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 446 tattgagtggtgacgttcgaatgaggaagcggttcgacccggtgcgaatc 505
|||||
Db 374 TATTGTAATGTGCTGCCACATGAAAGGTTGTGTCTGCTCAGAGGTTACGC 433
QY 506 gtgatcacctgggagctgacgatgctgtctctgtgtcctggaacacacacct 565
|||||
Db 434 ACGGCTACTGCGTCCCTGCTTCTATTGCTACATGCTGCTCGGAGCTACGAATCT 493
QY 566 gattcagagttctatgattcgacatcgaaatggtcgaaagtgltggtccatcgatgca 625
|||||
Db 494 TGTTAGCGGCTGCTGCTGCTTGTGTGATAGATCCCATTTGCTATTACCGGTCA 553
QY 626 tattcagagtgccagattggttcgaagcttctccagaaacgcat 671
|||||
Db 554 AGTGCCGAGGAGATGATGTGCTGATGCTTCAAGAACTCTCT 599

RESULT 14
AM033050 644 bp mRNA EST 15-SEP-1999
LOCUS EST276609 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC21L2, mRNA sequence.
ACCESSION AM033050
VERSION AM033050.1 GI:5891806
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 644)
Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D., and Giovannoni,J. Generation of ESTs from tomato callus tissue Unpublished (1999)
CONTACT: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
5 prime sequence.
FEATURES
source
1. .644
Location/Qualifiers
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC21L2"
/clone_1lb="tomato callus, TAMU"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Giovannoni Laboratory; cLEC - Cotyledons

of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 153 a 154 c 148 g 189 t

Query Match 2.4%; Score 51.6; DB 39; Length 644;
Best Local Similarity 51.8%; Pred. No. 0.00034;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 446 tatgtggtggtgacgttcgaatgagaagcgcgcgtttgtcagccggtgcaatc 505
|||||
Db 335 TATTGCTATATGCTCCACAGCATGACAGCGGTGCTGTGTCGACAGAGGTTACCG 394
QY 506 gtgtacacactggtgagcgtcagatgctgtcttctgtgtgcccggaaacacact 565
|||||
Db 395 ACGGCTACTGGTCCCTGGTGTGTTGTTGCTACATCTGGGCGGAGCTAGCATCT 454
QY 566 gattcaggtcttatgatcgtcgtcgaatggtgcaaggtgtgtcgtcgtcagca 625
|||||
Db 455 TGTACCGGCTGCTGCTGAGTGTGTTGATGATGATCCGATTTGCTATTACCGCTCA 514
QY 626 tatccgaatgcccgaattggttcgacgttcttcagagaaacgcat 671
|||||
Db 515 AGTCCGAGAGAGATGATTGATGATGATGATGATGATGATGATGATGATGATGAT 560

RESULT 15
BE681144 523 bp mRNA EST 11-SEP-2000
LOCUS BE681144
DEFINITION dg06d12.y1 Xenopus laevis gastrula non normalized Xenopus laevis
CDNA clone XENOPUS_SOURCE_ID:xlnnga002n24 5' similar to WP:R0334.3A
CE19658 ; mRNA sequence.
ACCESSION BE681144
VERSION BE681144.1 GI:10065702
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 523)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wyllie,T., Underwood,K., Theising,B., Bowers,Y., Person,
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
this library can be found through Research Genetics, visit their
web page at: <http://www.resgen.com/> Please reference the id listed
below when ordering this clone: Source lab clone id - xlnnga002n24
Seq primer: -40RP from Gibco
High quality sequence stop: 396.

FEATURES

Location/Qualifiers
1..523
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnnga002n24"
/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"

/Lab_host="Top-10 F"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
EcoRI-XhoI cut cDNA was then ligated into UniZap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
to biotinylated driver (prepared from the same library by
PCR) to Cot-omega of 11. After removal of hybrids and
excess driver by streptavidin sepharose chromatography,
the ss-phagemids were made double stranded and
electroporated into Top-10 F'. Original library
construction by Bruce Blumberg (Cho et al. 1991 Cell 67,
1111-1120). Note: This is a Xenopus Gene Collection (XGC)
library."

BASE COUNT 136 a 112 c 145 g 130 t

Query Match 2.4%; Score 51.2; DB 111; Length 523;
Best Local Similarity 50.4%; Pred. No. 0.00041;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 311 acgttgagaggttcagatgacacagctacgcagaacatattgacacttggagc 370
|||||
Db 16 AGGCTGCGAGGAGCAGAGAACCTGCTACGTGACACAAATCATTTGACAGGCGCTAGTGC 75
QY 371 tcaaggttgaaagcaattatgttgggttggtgacagccttaattccgacgttgatgc 430
|||||
Db 76 ACAAAATGTAAGTATATGTTGTCATGATGATGATGATGATGATGATGATGATGATGAT 135
QY 431 tctcgccaatcagatattggttggttcagcgttcgaatgagaagcgcgcgtttgc 490
|||||
Db 136 TCCGACGCTGCTGGATCAAGTATGTTGGATGGAATGAAATGAAACCGCTTCTATGC 195
QY 491 agccgtgacgaatcgttgatcaactggtgagcgtgcaatgctgtcttctgtgtgc 550
|||||
Db 196 AGCCTGCTGCTGGGCTATATCACTGCGACGCGACGAGATATGCTTTGTTGCTGTGACC 255
QY 551 tggaaaca 538
|||||
Db 256 AGGCCTCA 263

Search completed: March 17, 2001, 20:25:48
Job time: 1625 sec